```
                             GenCore version 6.3
                    Copyright (c) 1993 - 2010  Biocceleration Ltd.
OM protein - protein search, using sw model
Run on:      September 17, 2010, 11:52:25 ; Search time 1 Seconds
                                             (without alignments)
                                          0.057 Million cell updates/sec

Title:        US-10-587-841-6
Perfect score: 1195
Sequence:     1 MPWTILLFAAGSLAIPAPSI.........PTSTSSSPETPEFSTFRACQ 230
Scoring table: BLOSUM62
              Gapop 10.0 , Gapext 0.5


Searched:     1 seqs, 248 residues


Total number of hits satisfying chosen parameters:      1


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :      seq1446.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
                                              SUMMARIES
                   %
Result           Query
  No.    Score  Match Length DB  ID                          Description
-----------------------------------------------------------------------------
    1     568   47.5   248  1  PCT-US01-16450A-1446          Sequence 1446, Ap
                                       ALIGNMENTS
RESULT 1
PCT-US01-16450A-1446
; Sequence 1446, Application PC/TUS0116450A
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA131PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/16450A
;  CURRENT FILING DATE:  2001-05-18
;  PRIOR APPLICATION NUMBER: 60/205,515
;  PRIOR FILING DATE: 2000-05-19
;  NUMBER OF SEQ ID NOS: 2820
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1446
;  LENGTH: 248
;  TYPE: PRT
;  ORGANISM: Homo sapiens
PCT-US01-16450A-1446

  Query Match             47.5%;  Score 568;  DB 1;  Length 248;
  Best Local Similarity   99.1%;  Pred. No. 0;
  Matches  112;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps     0;

Qy       114 VPTWILVLSLSLAGALFLLAGLVAVALVVRKVKLRNLQKKRDRESCWAQINFDSTDMSFD 173
             :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 MPTWILVLSLSLAGALFLLAGLVAVALVVRKVKLRNLQKKRDRESCWAQINFDSTDMSFD 60

Qy       174 NSLFTVSAKTMPEEDPATLDDHSGTTATPSNSRTRKRPTSTSSSPETPEFSTF 226
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 NSLFTVSAKTMPEEDPATLDDHSGTTATPSNSRTRKRPTSTSSSPETPEFSTF 113


Search completed: September 17, 2010, 11:52:25
Job time : 1 secs
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